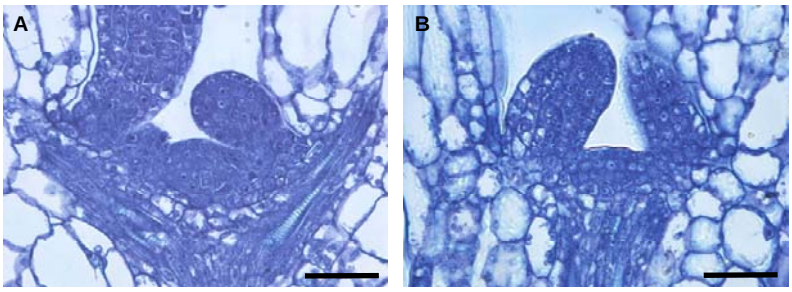
SUPPLEMENTAL MATERIAL



Supplemental Figure 1. Apical meristems of En-2 and *icu4-1/icu4-1* 3-day-old seedlings show comparable size and shape. Longitudinal sections are shown from (A) En-2 and (B) *icu4-1/icu4-1* seedlings. Scale bars indicate 50 mm.

Supplemental Table 1. Mutations used in this work

Mutation	Genetic background	NASC accession number	Mutagen	Origin
icu4-1	En-2	N400	Unknown	1
icu4-2	En-2	N401	Unknown	1
icu4-3	Col-0	N517186	T-DNA	2
icu4-4	Col-0	N513134	T-DNA	2
athb8-3	Col-0	N523733	T-DNA	2
athb8-4	Col-0	N565586	T-DNA	2
athb8-5	Col-0	N579212	T-DNA	2
hst-1	L*er*	N3811	Diepoxybutane	3, 4
crc-1	L*er*	N3814	EMS	5
pkl-1	Col*	N3840	EMS	6, 7
kan1-2	L*er*	-	EMS	8, 9

*As indicated in the NASC database. [1]Serrano-Cartagena et al. (2000). [2]Alonso et al. (2003). [3]Telfer and Poethig (1998). [4]Bollman et al. (2003). [5]Alvarez and Smyth (1999). [6]Ogas et al. (1997). [7]Ogas et al. (1999). [8]Eshed et al. (1999). [9]Kerstetter et al. (2001).

Supplemental Table 2. Primer pairs used in this work

Purpose	Marker/Gene	BAC	Oligonucleotide sequences (5´→3´)		PCR product size (bp)
			Forward primer (label, if any)	Reverse primer	
Linkage analysis	*nga280*	F14J16	GGTGCACTTTTTATGGAGCC (6-FAM)	CTGATCTCACGGACAATAGTGC	105 (Col-0); 85 (En-2)
	nga128	F7A10	GGTCTGTTGATGTCGTAAGTCG (TET)	CCCTCCCTAAAGGTTTCAAGAT	162 (En-2); 181 (Col-0)
	SM63	F8L10	ATGCTGGACCGAAGGCTACC	CAGTCACAGAGCTCATAAACAG	178 (En-2); 154 (Col-0)
	SNP375	F14I3	GCACATTCACAGAAAGTTTCTG (HEX)	TACTTCATTCTGCGAAGTTAGG	201 (En-2); 219 (Col-0)
	SNP17	F1I21	GATGTAATGAACCCAAGTCCTG	GATTCAGGGTTTGTTCTTACTG	98+171 (En-2)[1]; 269 (Col-0)
	F11M15	F11M15	GCCGTGTTTTAATCGCCTCAG	GAGGCTTCTCAATTCTCTTTCG	839 (En-2); 832 (Col-0)
	F19K6	F19K6	TGGGTAAAGTGGCATTGATCAC	AATTACGAATATCAGGGCACGG	302 (En-2 and Col-0)[2]
Confirmation of T-DNA insertions	*ICU4*	F5F19	TATCCCTCTTGATTCCGCAAAG	LBa1 and LBb1[3]	1561; 1363
	ICU4	F5F19	LBa1 and LBb1[3]	ATGGAACCAACTTTATGGTTCAC	795; 597
	ICU4	F5F19	AACAATGTTCCTTGCTTGGGAA	LBa1 and LBb1[3]	640; 442
	ICU4	F5F19	LBa1 and LBb1[3]	CAGAGGTGTAACGTAACAGCC	1302; 1104
	ATHB-8	T16I18	GCGTCGGCTCTAGACGTAGGG	LBa1 and LBb1[3]	634; 436
	ATHB-8	T16I18	LBa1 and LBb1[3]	TCTGCTTCATGTTCCTCAACTGG	Not amplified
	ATHB-8	T16I18	AGCTTGAGAGCTTGGGGCACT	LBa1 and LBb1[3]	Not amplified
	ATHB-8	T16I18	LBa1 and LBb1[3]	GAAGCTCACACTCTCGCTCGC	682; 484
	ATHB-8	T16I18	CCGTCGTTGAACCTTTTAAAGACCT	LBa1 and LBb1[3]	Not amplified
	ATHB-8	T16I18	LBa1 and LBb1[3]	AGCAGGGGAATTTGGCTACCA	657; 459
RT-PCR	*ICU4*	F5F19	ATGCTAGTCCTGCAGGACTTTT	CAACCATGAGAAATAGCGATGAT	130
	OTC	F1B16	TGAAGGGACAAAGGTTGTGTATGTT	ATCATCGCTATTTCTCATGGTTG	95

qRT-PCR	*YAB3*	F6N15	TCACGGTCACCGACAAAAGGT	GTCCTTGCTGTGAGTGTTCCT	91
	KAN1	MQK4	GCCATGAAAGAGCAACTCCAAA	ACATGTGAAGAGCCATTTGCAG	86
	KAN2	F27G20	GACGACTGGATGTTCGATATGA	AATTCTTCCGGAGAAGCACGTT	109
	KNAT1	F9M13	CCATTCAGGAAGCAATGGAGTT	ACTCTTCCCATCAGGATTGTTGA	101
	KNAT2	F24J13	CTCTTTCAGATGATGGTGCGGTT	GCGTAGTAGCTGGTCCTTCAGATC	119
	KNAT6	F28C11	GGGAGTTTCTGAGGATGGTGTAA	TTTGAGGTCCCGGTCTTCACA	105
	OTC	F1B16	TGAAGGGACAAAGGTTGTGTATGTT	ATCATCGCTATTTCTCATGGTTG	95
	ICU4	F5F19	AGAACCGAAGATGTAGAGAGAAA	TTGACGGAAGTAGCTGTTTTCAT	158
	PNH	MQD19	TCAACCAACAAGAGAGCTAATGTTT	GTGAATCCATACATCTCTTGGAA	90
Genomic DNA amplification and cycle sequencing	*ICU4*	F5F19	TCAGAGAGATGCTAGTCCTGC	CAGAGGTGTAACGTAACAGCC	760 (gDNA); 386 (cDNA)
	ICU4	F5F19	GCTTCGTTTCGAGGTGGAATC	GTTTCTTCTGCAATGGACAAAAG	1384 (gDNA); 1058 (cDNA)
	ICU4	F5F19	GCGTCAGCTCAAGCAAATAGC	TCTGGCTGAGAGCTCTTAAGG	98 (gDNA and cDNA)
	ICU4	F5F19	TATCCCTCTTGATTCCGCAAAG	ACAAAGGACCAATTGATGAACAC	1090 (gDNA); 747 (cDNA)
	ICU4	F5F19	CTTCAAGGCGGGATATGTCTC	ATGGAACCAACTTTATGGTTCAC	679 (gDNA and cDNA)
	ICU4	F5F19	GTTTCTGAGGGAGCATAGGTC	TTCGGTTTGGGCTAGATACTTC	635 (gDNA); 389 (cDNA)
	ICU4	F5F19	AGAACCGAAGATGTAGAGAGAAA	TTGACGGAAGTAGCTGTTTTCAT	158 (cDNA)
In situ	*ICU4*	F5F19	TTGATGCGTATCTAGCAGCAGCAG	CGAAACGAAGCATCGATTGGAGC	435

Oligonucleotides labeled with HEX (4, 7, 2', 4', 5', 7'-Hexachloro-6-carboxyfluorescein), TET (4, 7, 2', 7'-Tetrachloro-6-carboxyfluorescein) or 6-FAM (6-Carboxyfluorescein) phosphoramidites are indicated. Primers were designed based on the Col-0 genomic sequence available at MIPS (http://mips.gsf.de/proj/thal/db/index.html). [1]Two fragments of the indicated sizes were obtained after restriction with *Hinf*I of the PCR amplification product. [2]The nucleotide in position 42506 of F19K6 is a T in En-2 and an A in Col-0. [3]PCR amplifications to confirm the presence of a T-DNA insertion were carried out using three primers, which included LBa1 (5'-TGGTTCACGTAGTGGGCCATCG-3') and LBb1 (5'-GCGTGGACCGCTTGCTGCAACT-3'). Two products of the sizes shown were obtained from each amplification.